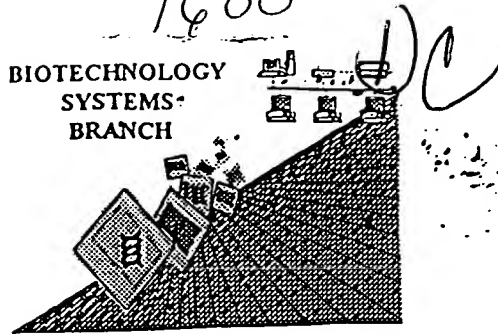


Re-run

1600
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/831758
Source: PCT 09
Date Processed by STIC: 10/18/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/831758 |
|--|---|--------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT | | |
| 1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping." | |
| 2 <input type="checkbox"/> Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 <input type="checkbox"/> Misaligned Amino Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. | |
| 4 <input type="checkbox"/> Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 <input type="checkbox"/> Variable Length | Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 <input type="checkbox"/> PatentIn 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 7 <input type="checkbox"/> Skipped Sequences (OLD RULES) | Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 <input type="checkbox"/> Skipped Sequences (NEW RULES) | Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000 | |
| 9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 10 <input type="checkbox"/> Invalid <213> Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence | |
| 11 <input checked="" type="checkbox"/> Use of <220> | Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) | |
| 12 <input type="checkbox"/> PatentIn 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 <input type="checkbox"/> Misuse of n | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide. | |

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
TIME: 09:51:48

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

Does Not Comply
Corrected Diskette Needed

2 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W--> 3 <120> TITLE OF INVENTION: Novel Protein and its DNA
W--> 4 <130> FILE REFERENCE: 2568WOOP

C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/831,758

C--> 5 <141> CURRENT FILING DATE: 2001-08-17

Does Not Comply
Corrected Diskette Needed

5 <150> PRIOR APPLICATION NUMBER: JP 10-323759

6 <151> PRIOR FILING DATE: 1998-11-13

7 <150> PRIOR APPLICATION NUMBER: JP 11-060030

8 <151> PRIOR FILING DATE: 1999-03-08

9 <150> PRIOR APPLICATION NUMBER: JP 11-106812

10 <151> PRIOR FILING DATE: 1999-04-14

11 <150> PRIOR APPLICATION NUMBER: JP 11-166672

12 <151> PRIOR FILING DATE: 1999-06-14

13 <150> PRIOR APPLICATION NUMBER: JP 11-221640

14 <151> PRIOR FILING DATE: 1999-08-04

15 <150> PRIOR APPLICATION NUMBER: JP 11-259818

16 <151> PRIOR FILING DATE: 1999-09-14

W--> 17 <160> NUMBER OF SEQ ID: 58

W--> 18 <210> SEQ ID NO: 1

19 <211> LENGTH: 180

20 <212> TYPE: PRT

21 <213> ORGANISM: Human

W--> 22 <400> SEQUENCE: 1

23 Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr

24 1 5 10 15

25 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met

26 20 25 30

27 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg

28 35 40 45

29 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp

30 50 55 60

31 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys

32 65 70 75 80

33 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val

34 85 90 95

35 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser

36 100 105 110

37 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro

38 115 120 125

39 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu

40 130 135 140

41 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu

42 145 150 155 160

43 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln

44 165 170 175

45 Lys Gln Ser Arg

46 180

Errored: "Artificial Sequence"
in field 213; mandatory
explanation in field 220 is
required.

See page 2 of 9.
See Error Summary Sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
TIME: 09:51:48

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

```

47 <210> SEQ ID NO: 2
48 <211> LENGTH: 540
49 <212> TYPE: DNA
50 <213> ORGANISM: Human
W--> 51 <400> SEQUENCE: 2
C--> 52 atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttggtta 60
53 acatcaaaca ttttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat 120
54 tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag 180
55 gaattaaaag attggggacc aaaaaatggtt attaagatga gtacacctgc agtcaataaa 240
56 atgccacact ccttcgcca cttgccattg agatttgga ggaacgttca agaagaaaga 300
57 agtgctggag caacagccaa cctgcctctg agatctgga agaaataagg ggtgagcctc 360
58 gtgagacgtg ttctaacct gcccaaaagg tttgggagaa caacaacagc caaaagtgtc 420
59 tgcaggatgc tgagtgtatt gtgtcaagga tccatgcatt caccatgtgc caatgactta 480
60 ttttactcca tgacctgcca gcaccaagaa atccagaatc ccgatcaaaa acagtcaagg 540
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 27
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence
W--> 65 <220> FEATURE:
66 <223> OTHER INFORMATION:
W--> 67 <400> SEQUENCE: 3
C--> 68 gggctgcaca tagagactta atttttag 27
69 <210> SEQ ID NO: 4
70 <211> LENGTH: 27
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
W--> 73 <220> FEATURE:
74 <223> OTHER INFORMATION:
W--> 75 <400> SEQUENCE: 4
C--> 76 ctagaccacc tctatataac tgcccat 27
77 <210> SEQ ID NO: 5
78 <211> LENGTH: 30
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
W--> 81 <220> FEATURE:
82 <223> OTHER INFORMATION:
W--> 83 <400> SEQUENCE: 5
C--> 84 gcacatagag acttaatttt agatttagac 30
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 27
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
W--> 89 <220> FEATURE:
90 <223> OTHER INFORMATION:
W--> 91 <400> SEQUENCE: 6
C--> 92 catgcacttt gactggtttc caggtat 27
93 <210> SEQ ID NO: 7
94 <211> LENGTH: 27
95 <212> TYPE: DNA

```

If 213 "Artificial Sequence"
Then 223 mandatory explanation

If 213 "Artificial Sequence"
Then 223 mandatory explanation.

Same...

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
TIME: 09:51:48

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10182001\I831758.raw

```

96 <213> ORGANISM: Artificial Sequence
W--> 97 <220> FEATURE:
98 <223> OTHER INFORMATION:
W--> 99 <400> SEQUENCE: 7
C--> 100 cagcttttagg gacaggctcc aggtttc 27
101 <210> SEQ ID NO: 8
102 <211> LENGTH: 196
103 <212> TYPE: PRT
104 <213> ORGANISM: Human
W--> 105 <400> SEQUENCE: 8
106 Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr
107 1 5 10 15
108 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met
109 20 25 30
110 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
111 35 40 45
112 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
113 50 55 60
114 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
115 65 70 75 80
116 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
117 85 90 95
118 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
119 100 105 110
120 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
121 115 120 125
122 Gln Arg Phe Gly Arg Thr Thr Ala Lys Ser Val Cys Arg Met Leu
123 130 135 140
124 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
125 145 150 155 160
126 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
127 165 170 175
128 Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu
129 180 185 190
130 Lys Gln Glu Lys
131 195
132 <210> SEQ ID NO: 9
133 <211> LENGTH: 588
134 <212> TYPE: DNA
135 <213> ORGANISM: Human
W--> 136 <400> SEQUENCE: 9
C--> 137 atggaaatta tttcatcaaa actattcatt ttattgactt tagccacttc aagcttggtta 60
138 acatcaaaca ttttttgtgc agatgaatta gtgatgtcca atcttcacag caaagaaaat 120
139 tatgacaaat attctgagcc tagaggatac ccaaaagggg aaagaagcct caattttgag 180
140 gaattaaaag attggggacc aaaaaatggtt attaagatga gtacacctgc agtcaataaa 240
141 atgccacact ccttgcgcaa cttgccattg agatttgga ggaacgttca agaagaaaga 300
142 agtgctggag caacagccaa cctgcctctg agatctggaa gaaatatgga ggtgagcctc 360
143 gtgagacgtg ttctaacct gcccaaaagg ttggggagaa caacaacagc caaaagtgtc 420
144 tgcaggatgc tgagtgattt gtgtcaagga tccatgcatt caccatgtgc caatgactta 480

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001

TIME: 09:51:48

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10182001\I831758.raw

```

145 ttttactcca tgacctgcca gcaccaagaa atccagaatc ccgatcaaaa acagtcaagg 540
146 agactgctat tcaagaaaat agatgatgca gaattgaaac aagaaaaa 588
147 <210> SEQ ID NO: 10
148 <211> LENGTH: 27
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
W--> 151 <220> FEATURE:
152 <223> OTHER INFORMATION:
W--> 153 <400> SEQUENCE: 10
C--> 154 gcctagagga gatctaggct gggagga 27
155 <210> SEQ ID NO: 11
156 <211> LENGTH: 27
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
W--> 159 <220> FEATURE:
160 <223> OTHER INFORMATION:
W--> 161 <400> SEQUENCE: 11
C--> 162 gggaggaaca tggaagaaga aaggagc 27
163 <210> SEQ ID NO: 12
164 <211> LENGTH: 27
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
W--> 167 <220> FEATURE:
168 <223> OTHER INFORMATION:
W--> 169 <400> SEQUENCE: 12
C--> 170 gatggtgaat gcatggactg ctggagc 27
171 <210> SEQ ID NO: 13
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
W--> 175 <220> FEATURE:
176 <223> OTHER INFORMATION:
W--> 177 <400> SEQUENCE: 13
C--> 178 ttctctcccaa atctcagtgg caggttg 27
179 <210> SEQ ID NO: 14
180 <211> LENGTH: 196
181 <212> TYPE: PRT
182 <213> ORGANISM: Bovine
W--> 183 <400> SEQUENCE: 14
184 Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu Met Leu Ala Thr
185 1 5 10 15
186 Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Thr Asp Glu Ser Arg Met
187 20 25 30
188 Pro Asn Leu Tyr Ser Lys Lys Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
189 35 40 45
190 Gly Asp Leu Gly Trp Glu Lys Glu Arg Ser Leu Thr Phe Glu Glu Val
191 50 55 60
192 Lys Asp Trp Ala Pro Lys Ile Lys Met Asn Lys Pro Val Val Asn Lys
193 65 70 75 80

```

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
 TIME: 09:51:48

Input Set : A:\PTO.MH.txt
 Output Set: N:\CRF3\10182001\I831758.raw

```

194 Met Pro Pro Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Met
195                      85                      90                      95
196 Glu Glu Glu Arg Ser Thr Arg Ala Met Ala His Leu Pro Leu Arg Leu
197                      100                      105                      110
198 Gly Lys Asn Arg Glu Asp Ser Leu Ser Arg Trp Val Pro Asn Leu Pro
199                      115                      120                      125
200 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Ile Thr Lys Thr Leu
201                      130                      135                      140
202 Ser Asn Leu Leu Gln Gln Ser Met His Ser Pro Ser Thr Asn Gly Leu
203 145                      150                      155                      160
204 Leu Tyr Ser Met Ala Cys Gln Pro Gln Glu Ile Gln Asn Pro Gly Gln
205                      165                      170                      175
206 Lys Asn Leu Arg Arg Arg Gly Phe Gln Lys Ile Asp Asp Ala Glu Leu
207                      180                      185                      190
208 Lys Gln Glu Lys
209                      195

```

```

211 <210> SEQ ID NO: 15
212 <211> LENGTH: 588
213 <212> TYPE: DNA
214 <213> ORGANISM: Bovine

```

W--> 215 <400> SEQUENCE: 15

```

C--> 216 atggaaatta ttctattaac acgattcatt ttattgatgt tagccacttc aagcttggtta 60
217 acatcaaaca tcttctgcac agacgaatca aggatgccca atctttacag caaaaagaat 120
218 tatgacaaat attccgagcc tagaggagat ctaggctggg agaaagaaag aagtcttact 180
219 tttgaagaag taaaagattg ggctccaaaa attaagatga ataaacctgt agtcaacaaa 240
220 atgccacctt ctgcagccaa cctgccactg agatttgga ggaacatgga agaagaaagg 300
221 agcactaggg cgatggccca cctgcctctg agactcggaa aaaatagaga ggacagcctc 360
222 tccagatggg tcccaaattc gccccagagg ttggaagaa caacaacagc caaaagcatt 420
223 accaagaccc tgagtaattt gctccagcag tccatgcatt caccatctac caatgggcta 480
224 ctctactcca tggcctgccg gcccgaagaa atccagaatc ctggtcaaaa gaacctaagg 540
225 agacggggat tccagaaaat agatgatgca gaattgaaac aagaaaaa 588

```

```

227 <210> SEQ ID NO: 16
228 <211> LENGTH: 27
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence

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W--> 231 <220> FEATURE:

232 <223> OTHER INFORMATION:

W--> 233 <400> SEQUENCE: 16

```

C--> 234 ccctggggct tcttctgtct tctatgt 27

```

```

235 <210> SEQ ID NO: 17
236 <211> LENGTH: 26
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence

```

W--> 239 <220> FEATURE:

240 <223> OTHER INFORMATION:

W--> 241 <400> SEQUENCE: 17

```

C--> 242 agcgattcat ttattgact ttagca 26

```

```

243 <210> SEQ ID NO: 18
244 <211> LENGTH: 203

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VERIFICATION SUMMARY

DATE: 10/18/2001

PATENT APPLICATION: US/09/831,758

TIME: 09:51:49

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10182001\I831758.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:17 M:283 W: Missing Blank Line separator, <160> field identifier
L:18 M:283 W: Missing Blank Line separator, <210> field identifier
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:65 M:283 W: Missing Blank Line separator, <220> field identifier
L:67 M:283 W: Missing Blank Line separator, <400> field identifier
L:68 M:112 C: (48) String data converted to lower case,
L:73 M:283 W: Missing Blank Line separator, <220> field identifier
L:75 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:112 C: (48) String data converted to lower case,
L:81 M:283 W: Missing Blank Line separator, <220> field identifier
L:83 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:112 C: (48) String data converted to lower case,
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:92 M:112 C: (48) String data converted to lower case,
L:97 M:283 W: Missing Blank Line separator, <220> field identifier
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:100 M:112 C: (48) String data converted to lower case,
L:105 M:283 W: Missing Blank Line separator, <400> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:137 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9
L:151 M:283 W: Missing Blank Line separator, <220> field identifier
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:154 M:112 C: (48) String data converted to lower case,
L:159 M:283 W: Missing Blank Line separator, <220> field identifier
L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:162 M:112 C: (48) String data converted to lower case,
L:167 M:283 W: Missing Blank Line separator, <220> field identifier
L:169 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:112 C: (48) String data converted to lower case,
L:175 M:283 W: Missing Blank Line separator, <220> field identifier
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:178 M:112 C: (48) String data converted to lower case,
L:183 M:283 W: Missing Blank Line separator, <400> field identifier
L:215 M:283 W: Missing Blank Line separator, <400> field identifier
L:216 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=15
L:231 M:283 W: Missing Blank Line separator, <220> field identifier
L:233 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:112 C: (48) String data converted to lower case,

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001
TIME: 09:51:49

Input Set : A:\PTO.MH.txt
Output Set : N:\CRF3\10182001\I831758.raw

L:239 M:283 W: Missing Blank Line separator, <220> field identifier
L:241 M:283 W: Missing Blank Line separator, <400> field identifier
L:242 M:112 C: (48) String data converted to lower case,
L:247 M:283 W: Missing Blank Line separator, <400> field identifier
L:278 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=19
L:294 M:283 W: Missing Blank Line separator, <220> field identifier
L:296 M:283 W: Missing Blank Line separator, <400> field identifier
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:297 M:112 C: (48) String data converted to lower case,
L:302 M:283 W: Missing Blank Line separator, <220> field identifier
L:304 M:283 W: Missing Blank Line separator, <400> field identifier
L:305 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:305 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:305 M:112 C: (48) String data converted to lower case,
L:310 M:283 W: Missing Blank Line separator, <220> field identifier
L:312 M:283 W: Missing Blank Line separator, <400> field identifier
L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:313 M:112 C: (48) String data converted to lower case,
L:318 M:283 W: Missing Blank Line separator, <220> field identifier
L:320 M:283 W: Missing Blank Line separator, <400> field identifier
L:321 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:321 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:321 M:112 C: (48) String data converted to lower case,
L:326 M:283 W: Missing Blank Line separator, <220> field identifier
L:328 M:283 W: Missing Blank Line separator, <400> field identifier
L:329 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:329 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:329 M:112 C: (48) String data converted to lower case,
L:334 M:283 W: Missing Blank Line separator, <220> field identifier
L:336 M:283 W: Missing Blank Line separator, <400> field identifier
L:337 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:337 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:337 M:112 C: (48) String data converted to lower case,
L:342 M:283 W: Missing Blank Line separator, <220> field identifier
L:344 M:283 W: Missing Blank Line separator, <400> field identifier
L:345 M:112 C: (48) String data converted to lower case,
L:350 M:283 W: Missing Blank Line separator, <220> field identifier
L:352 M:283 W: Missing Blank Line separator, <400> field identifier
L:353 M:112 C: (48) String data converted to lower case,

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,758

DATE: 10/18/2001

TIME: 09:51:49

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10182001\I831758.raw

L:361 M:112 C: (48) String data converted to lower case,
L:369 M:112 C: (48) String data converted to lower case,
L:377 M:112 C: (48) String data converted to lower case,
L:385 M:112 C: (48) String data converted to lower case,
L:393 M:112 C: (48) String data converted to lower case,
L:428 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=34
L:445 M:112 C: (48) String data converted to lower case,
L:453 M:112 C: (48) String data converted to lower case,
L:518 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=38
L:572 M:112 C: (48) String data converted to lower case,
L:578 M:112 C: (48) String data converted to lower case,
L:584 M:112 C: (48) String data converted to lower case,
L:590 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=45
L:600 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=46
L:611 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=47
L:625 M:112 C: (48) String data converted to lower case,
L:633 M:112 C: (48) String data converted to lower case,
L:670 M:112 C: (48) String data converted to lower case,

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/831,758

DATE: 09/27/2001

TIME: 11:58:46

Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

2 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W--> 3 <120> TITLE OF INVENTION: Novel Protein and its DNA
W--> 4 <130> FILE REFERENCE: 2568WO0P
C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/831,758
C--> 5 <141> CURRENT FILING DATE: 2001-08-17
5 <150> PRIOR APPLICATION NUMBER: JP 10-323759
6 <151> PRIOR FILING DATE: 1998-11-13
7 <150> PRIOR APPLICATION NUMBER: JP 11-060030
8 <151> PRIOR FILING DATE: 1999-03-08
9 <150> PRIOR APPLICATION NUMBER: JP 11-106812
10 <151> PRIOR FILING DATE: 1999-04-14
11 <150> PRIOR APPLICATION NUMBER: JP 11-166672
12 <151> PRIOR FILING DATE: 1999-06-14
13 <150> PRIOR APPLICATION NUMBER: JP 11-221640
14 <151> PRIOR FILING DATE: 1999-08-04
15 <150> PRIOR APPLICATION NUMBER: JP 11-259818
16 <151> PRIOR FILING DATE: 1999-09-14
E--> 17 <160> NUMBER OF SEQ ID: 58

ERRORED SEQUENCES

210 <210> SEQ ID NO: 15
211 <211> LENGTH: 588
212 <212> TYPE: DNA
213 <213> ORGANISM: Bovine
W--> 214 <400> SEQUENCE: 15
E--> 214 15
E--> 215 <210> SEQ ID NO: 15

check sequence 15 for actual sequence listing

VERIFICATION SUMMARY

DATE: 09/27/2001

PATENT APPLICATION: US/09/831,758

TIME: 11:58:47

Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
 L:4 M:283 W: Missing Blank Line separator, <130> field identifier
 L:5 M:270 C: Current Application Number differs, Replaced Current Application No
 L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:17 M:283 W: Missing Blank Line separator, <160> field identifier
 L:18 M:283 W: Missing Blank Line separator, <210> field identifier
 L:22 M:283 W: Missing Blank Line separator, <400> field identifier
 L:51 M:283 W: Missing Blank Line separator, <400> field identifier
 L:52 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=2
 L:65 M:283 W: Missing Blank Line separator, <220> field identifier
 L:67 M:283 W: Missing Blank Line separator, <400> field identifier
 L:68 M:112 C: (48) String data converted to lower case,
 L:73 M:283 W: Missing Blank Line separator, <220> field identifier
 L:75 M:283 W: Missing Blank Line separator, <400> field identifier
 L:76 M:112 C: (48) String data converted to lower case,
 L:81 M:283 W: Missing Blank Line separator, <220> field identifier
 L:83 M:283 W: Missing Blank Line separator, <400> field identifier
 L:84 M:112 C: (48) String data converted to lower case,
 L:89 M:283 W: Missing Blank Line separator, <220> field identifier
 L:91 M:283 W: Missing Blank Line separator, <400> field identifier
 L:92 M:112 C: (48) String data converted to lower case,
 L:97 M:283 W: Missing Blank Line separator, <220> field identifier
 L:99 M:283 W: Missing Blank Line separator, <400> field identifier
 L:100 M:112 C: (48) String data converted to lower case,
 L:105 M:283 W: Missing Blank Line separator, <400> field identifier
 L:136 M:283 W: Missing Blank Line separator, <400> field identifier
 L:137 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=9
 L:151 M:283 W: Missing Blank Line separator, <220> field identifier
 L:153 M:283 W: Missing Blank Line separator, <400> field identifier
 L:154 M:112 C: (48) String data converted to lower case,
 L:159 M:283 W: Missing Blank Line separator, <220> field identifier
 L:161 M:283 W: Missing Blank Line separator, <400> field identifier
 L:162 M:112 C: (48) String data converted to lower case,
 L:167 M:283 W: Missing Blank Line separator, <220> field identifier
 L:169 M:283 W: Missing Blank Line separator, <400> field identifier
 L:170 M:112 C: (48) String data converted to lower case,
 L:175 M:283 W: Missing Blank Line separator, <220> field identifier
 L:177 M:283 W: Missing Blank Line separator, <400> field identifier
 L:178 M:112 C: (48) String data converted to lower case,
 L:183 M:283 W: Missing Blank Line separator, <400> field identifier
 L:214 M:283 W: Missing Blank Line separator, <400> field identifier
 L:214 M:252 E: No. of Seq. differs, <211>LENGTH:Input:588 Found:0 SEQ:15
 L:215 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:15
 L:219 M:283 W: Missing Blank Line separator, <400> field identifier
 L:220 M:112 C: (48) String data converted to lower case,
 M:112 Repeated in SeqNo=15

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,758

DATE: 09/27/2001

TIME: 11:58:47

Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

L:234 M:283 W: Missing Blank Line separator, <220> field identifier
L:236 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:112 C: (48) String data converted to lower case,
L:242 M:283 W: Missing Blank Line separator, <220> field identifier
L:244 M:283 W: Missing Blank Line separator, <400> field identifier
L:245 M:112 C: (48) String data converted to lower case,
L:250 M:283 W: Missing Blank Line separator, <400> field identifier
L:281 M:283 W: Missing Blank Line separator, <400> field identifier
L:282 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=19
L:297 M:283 W: Missing Blank Line separator, <220> field identifier
L:299 M:283 W: Missing Blank Line separator, <400> field identifier
L:300 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:300 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:300 M:112 C: (48) String data converted to lower case,
L:305 M:283 W: Missing Blank Line separator, <220> field identifier
L:307 M:283 W: Missing Blank Line separator, <400> field identifier
L:308 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:308 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:308 M:112 C: (48) String data converted to lower case,
L:313 M:283 W: Missing Blank Line separator, <220> field identifier
L:315 M:283 W: Missing Blank Line separator, <400> field identifier
L:316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:316 M:112 C: (48) String data converted to lower case,
L:321 M:283 W: Missing Blank Line separator, <220> field identifier
L:323 M:283 W: Missing Blank Line separator, <400> field identifier
L:324 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:324 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:324 M:112 C: (48) String data converted to lower case,
L:329 M:283 W: Missing Blank Line separator, <220> field identifier
L:331 M:283 W: Missing Blank Line separator, <400> field identifier
L:332 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:332 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:332 M:112 C: (48) String data converted to lower case,
L:337 M:283 W: Missing Blank Line separator, <220> field identifier
L:339 M:283 W: Missing Blank Line separator, <400> field identifier
L:340 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:340 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:340 M:112 C: (48) String data converted to lower case,
L:345 M:283 W: Missing Blank Line separator, <220> field identifier
L:347 M:283 W: Missing Blank Line separator, <400> field identifier
L:348 M:112 C: (48) String data converted to lower case,

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/831,758

DATE: 09/27/2001

TIME: 11:58:47

Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

L:353 M:283 W: Missing Blank Line separator, <220> field identifier
L:356 M:112 C: (48) String data converted to lower case,
L:364 M:112 C: (48) String data converted to lower case,
L:372 M:112 C: (48) String data converted to lower case,
L:380 M:112 C: (48) String data converted to lower case,
L:388 M:112 C: (48) String data converted to lower case,
L:396 M:112 C: (48) String data converted to lower case,
L:431 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=34
L:448 M:112 C: (48) String data converted to lower case,
L:456 M:112 C: (48) String data converted to lower case,
L:521 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=38
L:575 M:112 C: (48) String data converted to lower case,
L:581 M:112 C: (48) String data converted to lower case,
L:587 M:112 C: (48) String data converted to lower case,
L:593 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=45
L:603 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=46
L:614 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=47
L:628 M:112 C: (48) String data converted to lower case,
L:636 M:112 C: (48) String data converted to lower case,
L:673 M:112 C: (48) String data converted to lower case,
L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (58) Counted (59)

STATISTICS SUMMARY

PATENT APPLICATION: US/09/831,758

DATE: 09/27/2001

TIME: 11:58:47

Input Set : A:\Sequence Listing .txt

Output Set: N:\CRF3\09272001\I831758.raw

Application Serial Number: US/09/831,758

Alpha or Numeric: Numeric

Application Class:

Application File Date: 08-17-2001

Art Unit: PCT09

Software Application:

Total Number of Sequences: 59

Total Nucleotides: 9253

Total Amino Acids: 2059

Number of Errors: 3

Number of Warnings: 116

Number of Corrections: 362

MESSAGE SUMMARY

112 C: 180 ((48) String data converted to lower case)
203 E: 1 (No. of Seq. differs)
212 E: 1 ((34) Invalid or duplicate Sequence ID Number)
252 E: 1 (No. of Seq. differs)
258 W: 12 (Mandatory Feature missing)
270 C: 1 (Current Application Number differs)
271 C: 1 (Current Filing Date, differs)
283 W: 98 (Missing Blank Line separator)
341 W: 6 ((46) "n" or "Xaa" used)